

SEQUENCE LISTING

<110> Houston, Michael E.
Hodges, Robert

<120> Use of Coiled-Coil Structural Scaffold to Generate
Structure-Specific Peptides

<130> 003592-007

<150> US 60/211,892

<151> 2000-06-14

<150> US 60/213,387

<151> 2000-06-23

<160> 16

<170> PatentIn version 3.0

<210> 1

<211> 619

<212> PRT

<213> Streptococcus pneumoniae

<400> 1

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Met Asn Lys Lys Lys Met Ile Leu Thr Ser Leu Ala Ser Val Ala Ile
      5                      10                      15
Leu Gly Ala Gly Phe Val Ala Ser Gln Pro Thr Val Val Arg Ala Glu
      20                      25                      30
Glu Ser Pro Val Ala Ser Gln Ser Lys Ala Glu Lys Asp Tyr Asp Ala
      35                      40                      45
Ala Lys Lys Asp Ala Lys Asn Ala Lys Lys Ala Val Glu Asp Ala Gln
      50                      55                      60
Lys Ala Leu Asp Asp Ala Lys Ala Ala Gln Lys Lys Tyr Asp Glu Asp
      65                      70                      75                      80
Gln Lys Lys Thr Glu Glu Lys Ala Ala Leu Glu Lys Ala Ala Ser Glu
      85                      90                      95
Glu Met Asp Lys Ala Val Ala Ala Val Gln Gln Ala Tyr Leu Ala Tyr
      100                     105                     110

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Gln	Gln	Ala	Thr	Asp	Lys	Ala	Ala	Lys	Asp	Ala	Ala	Asp	Lys	Met	Ile	
		115					120					125				
Asp	Glu	Ala	Lys	Lys	Arg	Glu	Glu	Glu	Ala	Lys	Thr	Lys	Phe	Asn	Thr	
	130					135					140					
Val	Arg	Ala	Met	Val	Val	Pro	Glu	Pro	Glu	Gln	Leu	Ala	Glu	Thr	Lys	
	145				150					155					160	
Lys	Lys	Ser	Glu	Glu	Ala	Lys	Gln	Lys	Ala	Pro	Glu	Leu	Thr	Lys	Lys	
				165					170					175		
Leu	Glu	Glu	Ala	Lys	Ala	Lys	Leu	Glu	Glu	Ala	Glu	Lys	Lys	Ala	Thr	
			180					185					190			
Glu	Ala	Lys	Gln	Lys	Val	Asp	Ala	Glu	Glu	Val	Ala	Pro	Gln	Ala	Lys	
		195					200					205				
Ile	Ala	Glu	Leu	Glu	Asn	Gln	Val	His	Arg	Leu	Glu	Gln	Glu	Leu	Lys	
	210					215					220					
Glu	Ile	Asp	Glu	Ser	Glu	Ser	Glu	Asp	Tyr	Ala	Lys	Glu	Gly	Phe	Arg	
	225				230					235					240	
Ala	Pro	Leu	Gln	Ser	Lys	Leu	Asp	Ala	Lys	Lys	Ala	Lys	Leu	Ser	Lys	
				245					250					255		
Leu	Glu	Glu	Leu	Ser	Asp	Lys	Ile	Asp	Glu	Leu	Asp	Ala	Glu	Ile	Ala	
			260					265					270			
Lys	Leu	Glu	Asp	Gln	Leu	Lys	Ala	Ala	Glu	Glu	Asn	Asn	Asn	Val	Glu	
		275					280					285				
Asp	Tyr	Phe	Lys	Glu	Gly	Leu	Glu	Lys	Thr	Ile	Ala	Ala	Lys	Lys	Ala	
	290					295					300					
Glu	Leu	Glu	Lys	Thr	Glu	Ala	Asp	Leu	Lys	Lys	Ala	Val	Asn	Glu	Pro	
	305				310					315					320	
Glu	Lys	Pro	Ala	Pro	Ala	Pro	Glu	Thr	Pro	Ala	Pro	Glu	Ala	Pro	Ala	
				325					330					335		
Glu	Gln	Pro	Lys	Pro	Ala	Pro	Ala	Pro	Gln	Pro	Ala	Pro	Ala	Pro	Lys	
			340					345					350			
Pro	Glu	Lys	Pro	Ala	Glu	Gln	Pro	Lys	Pro	Glu	Lys	Thr	Asp	Asp	Gln	
		355					360					365				

Gln	Ala	Glu	Glu	Asp	Tyr	Ala	Arg	Arg	Ser	Glu	Glu	Glu	Tyr	Asn	Arg	370	375	380	
Leu	Thr	Gln	Gln	Gln	Pro	Pro	Lys	Ala	Glu	Lys	Pro	Ala	Pro	Ala	Pro	385	390	395	400
Lys	Thr	Gly	Trp	Lys	Gln	Glu	Asn	Gly	Met	Trp	Tyr	Phe	Tyr	Asn	Thr	405	410	415	
Asp	Gly	Ser	Met	Ala	Thr	Gly	Trp	Leu	Gln	Asn	Asn	Gly	Ser	Trp	Tyr	420	425	430	
Tyr	Leu	Asn	Ser	Asn	Gly	Ala	Met	Ala	Thr	Gly	Trp	Leu	Gln	Tyr	Asn	435	440	445	
Gly	Ser	Trp	Tyr	Tyr	Leu	Asn	Ala	Asn	Gly	Ala	Met	Ala	Thr	Gly	Trp	450	455	460	
Ala	Lys	Val	Asn	Gly	Ser	Trp	Tyr	Tyr	Leu	Asn	Ala	Asn	Gly	Ala	Met	465	470	475	480
Ala	Thr	Gly	Trp	Leu	Gln	Tyr	Asn	Gly	Ser	Trp	Tyr	Tyr	Leu	Asn	Ala	485	490	495	
Asn	Gly	Ala	Met	Ala	Thr	Gly	Trp	Ala	Lys	Val	Asn	Gly	Ser	Trp	Tyr	500	505	510	
Tyr	Leu	Asn	Ala	Asn	Gly	Ala	Met	Ala	Thr	Gly	Trp	Leu	Gln	Tyr	Asn	515	520	525	
Gly	Ser	Trp	Tyr	Tyr	Leu	Asn	Ala	Asn	Gly	Ala	Met	Ala	Thr	Gly	Trp	530	535	540	
Ala	Lys	Val	Asn	Gly	Ser	Trp	Tyr	Tyr	Leu	Asn	Ala	Asn	Gly	Ala	Met	545	550	555	560
Ala	Thr	Gly	Trp	Val	Lys	Asp	Gly	Asp	Thr	Trp	Tyr	Tyr	Leu	Glu	Ala	565	570	575	
Ser	Gly	Ala	Met	Lys	Ala	Ser	Gln	Trp	Phe	Lys	Val	Ser	Asp	Lys	Trp	580	585	590	
Tyr	Tyr	Val	Asn	Gly	Leu	Gly	Ala	Leu	Ala	Val	Asn	Thr	Thr	Val	Asp	595	600	605	
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<210> 2
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<220>
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<220>
 <221> MOD_RES
 <222> (2)
 <223> Nle

<400> 2

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Cys Xaa Gly Gly Gly Glu Ile Glu Ala Leu Lys Lys Glu Ile Glu Ala
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Leu Lys Lys Glu Ile Glu Ala Leu Lys Lys Glu Ile Glu Ala Leu Lys
20          25          30
Lys Glu Ile Glu Ala Leu Lys Lys
35          40

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<210> 3
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 <213> Artificial Sequence

<220>
 <223> hybrid sequence

<220>
 <221> MOD_RES
 <222> (2)
 <223> Nle

<400> 3

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Cys Xaa Gly Ile Glu Glu Leu Glu Lys Lys Ile Thr Glu Leu Lys Gln
1          5          10          15
Lys Ile Asp Ala Leu Glu Asn Gln Ile His Arg Leu Glu Gln Glu Ile
20          25          30
Lys Glu Leu Asp Glu Ser

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35

<210> 4
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<220>
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<220>
 <221> MOD_RES
 <222> (2)
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<400> 4

Cys Xaa Gly Leu Glu Glu Ala Glu Lys Lys Ala Thr Glu Ala Lys Gln
 1 5 10 15

Lys Val Asp Ala Leu Glu Asn Gln Val His Arg Leu Glu Gln Glu Leu
 20 25 30

Lys Glu Ile Asp Glu Ser
 35

<210> 5
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<220>
 <221> PEPTIDE
 <222> (4)..(20)
 <223> Amino acids 4, 5, 12, 16 and 20 are Xaa wherein Xaa = any a
 mino acid

<400> 5

Glu Glu Leu Xaa Xaa Lys Ile Asp Glu Leu Asp Xaa Glu Ile Ala Xaa
 1 5 10 15

Leu Glu Lys Xaa
 20

<210> 9
 <211> 27
 <212> PRT
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<220>
 <223> hybrid sequence

<400> 9

Glu Ala Glu Ile Lys Lys Leu Leu Glu Ile Ile Leu Asn Leu Ser Gln
 1 5 10 15

Glu Ile Ser Asn Leu Thr Ser Ala Leu Lys Gly
 20 25

<210> 10
 <211> 20
 <212> PRT
 <213> Streptococcus pneumoniae

<400> 10

Leu Glu Lys Asp Val Glu Asp Phe Lys Asn Ser Asp Gly Glu Gln Ala
 5 10 15

Glu Gln Val Leu
 20

<210> 11
 <211> 15
 <212> PRT
 <213> Streptococcus pneumoniae

<400> 11

Leu Glu Asp Asn Leu Lys Asp Ala Glu Thr Asn Asn Val Glu Asp
 1 5 10 15

<210> 12
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 <212> PRT
 <213> Streptococcus pneumoniae

<400> 12

Leu Ala Lys Lys Gln Thr Glu Leu Glu Lys
 1 5 10

<210> 13
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<220>
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<400> 13

Asp Val Glu Asp Phe Lys Asn Ser Asp Gly Glu Leu Glu Asp Asn Leu
 1 5 10 15

Lys Asp Ala Glu Thr Asn Asn Val Glu Asp Ala Lys Lys Gln Thr Glu
 20 25 30

Leu Glu Lys
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<210> 14
 <211> 35
 <212> PRT
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<220>
 <223> hybrid sequence

<400> 14

Asp Ile Glu Asp Leu Lys Asn Ser Ile Gly Glu Leu Glu Asp Asn Ile
 5 10 15

Lys Glu Leu Glu Thr Asn Ile Val Glu Leu Ala Lys Lys Ile Thr Glu
 20 25 30

Leu Glu Lys
 35

<210> 15
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 <212> PRT
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<220>
 <223> Coiled-coil scaffold

<220>

<221> PEPTIDE
 <222> (1)
 <223> Amino acid 1 is Xaa wherein Xaa = A and A can be I, L or V.

<220>
 <221> PEPTIDE
 <222> (2)..(7)
 <223> Amino acids 2, 3, 5-7 are Xaa wherein Xaa = any amino acid.

<220>
 <221> PEPTIDE
 <222> (4)
 <223> Amino acid 4 is Xaa wherein Xaa = D and D can be I, L or V.

<220>
 <221> PEPTIDE
 <222> (1)..(7)
 <223> Amino acids 1-7 can be repeated one or more times.

<400> 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5

<210> 16
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 <212> PRT
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<220>
 <223> Coiled-coil scaffold

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 <221> MOD_RES
 <222> (2)
 <223> Nle

<220>
 <221> PEPTIDE
 <222> (5)..(10)
 <223> Amino acids 5, 6, and 8-10 are Xaa wherein Xaa = any amino acid.

<220>
 <221> PEPTIDE
 <222> (4)..(10)
 <223> Amino acids 4-10 can be repeated one or more times.

<400> 16

Cys	Xaa	Gly	Ile	Xaa	Xaa	Leu	Xaa	Xaa	Xaa
1				5					10

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<210> 6
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<220>
 <223> consensus sequence

<400> 6

Glu Glu Leu Ser Asp Lys Ile Asp
 1 5

<210> 7
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 <212> PRT
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<220>
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<220>
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 <222> (2)
 <223> Nle

<400> 7

Cys Xaa Gly Glu Ile Glu Ala Leu Lys Lys Lys Ile Glu Glu Leu Ser
 1 5 10 15

Asp Lys Ile Asp Glu Leu Glu Lys Glu Ile Lys
 20 25

<210> 8
 <211> 21
 <212> PRT
 <213> Haemophilus influenzae

<400> 8

Ile Lys Lys Val Leu Glu Ile Gly Leu Asn Met Ser Gln Glu Ala Ser
 1 5 10 15

Asn Leu Thr Ser Ala
 20